

TTTATTAAAAAGGTGACAAATCTCTATCAATTCTCAGGAACTTCCTGAAGGAACTACCAATAT 630
 Leu Leu Lys Lys Val Thr Asn Asn Leu Tyr Gln Phe Ser Gly Asp Leu Pro Glu Gly Asn Tyr Gln Tyr

AAAGTGGCTTTAAATGATAGCTGGAATAATCCGAGTTACCCATCTGACAACATTAATTTAACAGTCCCTG 700
 Lys Val Ala Leu Asn Asp Ser Trp Asn Asn Pro Ser Tyr Pro Ser Asp Asn Ile Asn Leu Thr Val Pro

CCGGCGGTGCACACGTCACCTTTTTTCGTATATTCCGTCCACTCATGCAGTCTATGACACAATTAATAATCC 770
 Ala Gly Gly Ala His Val Thr Phe Ser Tyr Ile Pro Ser Thr His Ala Val Tyr Asp Thr Ile Asn Asn Pro

TAATGCGGATTTACAAGTAGAAAGCGGGGTTAAAACGGATCTCGTGACGGTTACTCTAGGGGAAGATCCA 840
 Asn Ala Asp Leu Gln Val Glu Ser Gly Val Lys Thr Asp Leu Val Thr Val Thr Leu Gly Glu Asp Pro

GATGTGAGCCATACTCTGTCCATTCAAACAGATGGCTATCAGGCAAAGCAGGTGATACCTCGTAATGTGC 910
 Asp Val Ser His Thr Leu Ser Ile Gln Thr Asp Gly Tyr Gln Ala Lys Gln Val Ile Pro Arg Asn Val

TAATTCATCACAGTACTACTATTCAGGAGATGATCTTGGGAATACCTATACACAGAAAGCAACAACCTT 980
 Leu Asn Ser Ser Gln³⁰⁹ Tyr^Y Tyr Tyr Ser Gly Asp Asp Leu Gly Asn Thr Tyr Thr Gln Lys Ala Thr Thr Phe

TAAAGTCTGGGCACCAACTTCTACTCAAGTAAATGTTCTTCTTTATGACAGTGCAACGGGTTCTGTAACA 1050
 VWAP
 Lys Val Trp Ala Pro Thr Ser Thr Gln Val Asn Val Leu Leu Tyr Asp Ser Ala Thr Gly Ser Val Thr

AAAATCGTACCTATGACGGCATCGGGCCATGGTGTGTGGGAAGCAACGGTTAATCAAAACCTTGAAAATT 1120
 Lys Ile Val Pro Met Thr Ala Ser Gly His Gly Val Trp Glu Ala Thr Val Asn Gln Asn Leu Glu Asn

FIGURE 1B

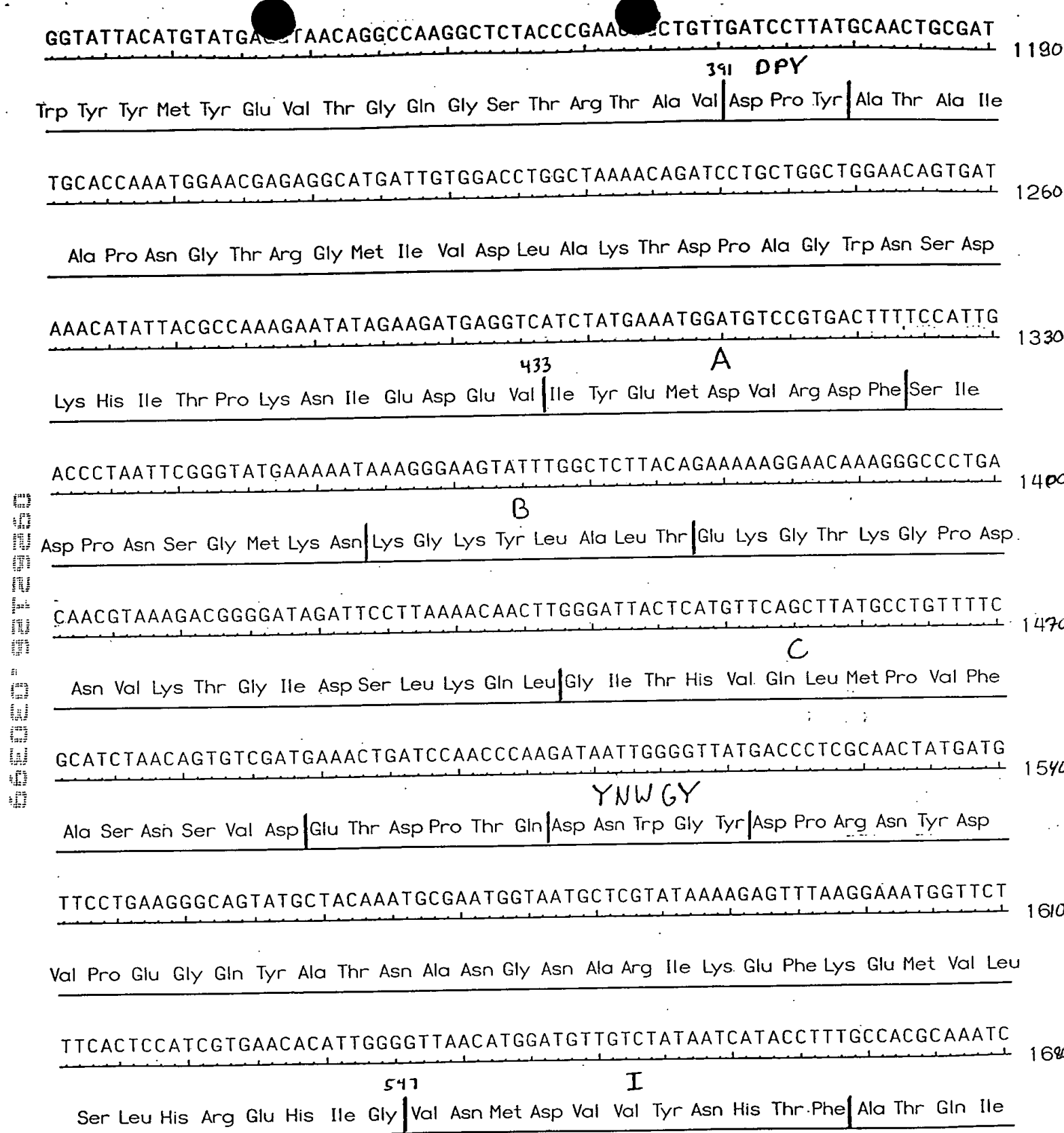


FIGURE 1C

TCTGACTTCGATAAA GTACCAGAATATTATTACCGTACGATGATCCAGGTAATTATACCAACGGATC

D

Ser Asp Phe Asp Lys Ile Val Pro Glu Tyr Tyr Tyr Arg Thr Met Ile Gln Val Ile Ile Pro Thr Asp

AGGTACTGGAAATGAAATTGCANGCNGAAAGGCCAATGGTTCAAAAATTTATTATTGATTCCCTTAAGTA

Gln Val Leu Glu Met Lys Leu ??? Ala Glu Arg Pro Met Val Gln Lys Phe Ile Ile Asp Ser Leu Lys Tyr

TTGGGTCAATGAGTATCATATTGACGGCTTCCGTTTTGACTTAATGGCGCTGCTTGGAAAAGACACGATG

II

Trp Val Asn Glu Tyr His Ile Asp Gly Phe Arg Phe Asp Leu Met Ala Leu Leu Gly Lys Asp Thr Met

TCCAAAGCTGCCTCGGAGCTTCATGCTATTAATCCAGGAATTGCACTTTACGGTGAGCCATGGACGGGTG

III

Ser Lys Ala Ala Ser Glu Leu His Ala Ile Asn Pro Gly Ile Ala Leu Tyr Gly Glu Pro Trp Thr Gly

GAACCTCTGCACTGCCAGATGATCAGCTTCTGACAAAAGGAGCTCAAAAAGGCATGGGAGTAGCGGTGTT

Gly Thr Ser Ala Leu Pro Asp Asp Gln Leu Leu Thr Lys Gly Ala Gln Lys Gly Met Gly Val Ala Val Phe

TAATGACAATTTACGAAACGCGTTGGACGGCAATGTCTTTGATTCTTCCGCTCAAGGTTTTGCGACAGGT

Asn Asp Asn Leu Arg Asn Ala Leu Asp Gly Asn Val Phe Asp Ser Ser Ala Gln Gly Phe Ala Thr Gly

GCAACAGGCTTAACTGATGCAATTAAGAATGGCGTTGAGGGGAGTATTAATGACTTTACCTCTTCACCAG

Ala Thr Gly Leu Thr Asp Ala Ile Lys Asn Gly Val Glu Gly Ser Ile Asn Asp Phe Thr Ser Ser Pro

GTGAGACAATTA ACTATGTCACAAGTCATGATAACTACACCCTTTGGGACAAAATAGCCCTAAGCAATCC

IV

Gly Glu Thr Ile Asn Tyr Val Thr Ser His Asp Asn Tyr Thr Leu Trp Asp Lys Ile Ala Leu Ser Asn Pro

FIGURE 1D

TAATGATTCCGAAGCGGATCGGATTAAAATGGATGAACTCGCACAAAGCAGTTGTTATGACCTCACAAGGC 2310
 Asn Asp Ser Glu Ala Asp Arg Ile Lys Met Asp Glu Leu Ala Gln Ala Val Val^E Met Thr Ser Gln Gly

GTTCCATTTCATGCAAGGCGGGGAAGAAATGCTTCGTANAAAAGGCGGCAACGACAATAGTTATAATGCAG 2380
 Val Pro Phe Met Gln Gly Gly Glu Glu Met Leu Arg ??? Lys Gly Gly Asn Asp Asn Ser Tyr Asn Ala

GCGATGCGGTCAATGAGTTTGATTGGAGCAGGAAAGCTCAATATCCAGATGTTTTCAACTATTATAGCGG 2450
 Gly Asp Ala Val Asn Glu Phe Asp Trp Ser Arg Lys Ala Gln Tyr Pro Asp Val Phe Asn Tyr Tyr Ser Gly

GCTAATCCACCTTCGTCTTGATCACCCAGCCTTCCGCATGACGACAGCTAATGAAATCAATAGCCACCTC 2520
 Leu Ile His Leu Arg Leu Asp His Pro Ala Phe Arg Met Thr Thr Ala Asn Glu Ile Asn Ser His Leu

CAATTCCTAAATAGTCCAGAGAACACAGTGGCCTATGAATTAAGTATCATGTTAATAAAGACAAATGGG 2590
 Gln Phe Leu Asn Ser Pro Glu Asn Thr Val Ala Tyr Glu Leu Thr Asp His Val Asn Lys Asp Lys Trp

GAAATATCATTGTTGTTTATAACCCAAATAAACTGTAGCAACCATCAATTTGCCGAGCGGGAAATGGGC 2660
 Gly Asn Ile Ile Val Val Tyr Asn Pro Asn Lys Thr Val Ala Thr Ile Asn Leu Pro Ser Gly Lys Trp Ala

AATCAATGCTACGAGCGGTAAGGTAGGAGAATCCACCCTTGGTCAAGCAGAGGGAAGTGTCCAAGTACCA 2730
 Ile Asn Ala Thr Ser Gly Lys Val Gly Glu Ser Thr Leu Gly Gln Ala Glu Gly Ser Val Gln Val Pro

GGTATATCTATGATGATCCTTCATCAAGAGGTAAGCCCAGACCACGGTAAAAAGTAATAGAAAA → 2794
 Gly Ile Ser Met Met Ile Leu His Gln Glu Val Ser Pro Asp His Gly Lys Lys

FIGURE 1E

	Majority			
	10	20	30	40
1	MAKKLIYVCLSVCLVLTWAFNVKGS	SAHADGNTTTTII	VHY	pullseqsig.seq.PRO
1	MLRYTRNALVLGSLVLLSGCD	NGSSSSSSSGNPDT		klebpnseqsig.seq.p
1	M	VSI	RRSFEA	subpull.seq.pro
	Majority			
	50	60	70	80
41	FCPAGDYQPWSLWMWPKDGGGA	EYDFNQPADSFG	AVASAD	pullseqsig.seq.PRO
35	PDNQDVVRL	PDVAVPGEAV	TAVENQAVIHLVD	klebpnseqsig.seq.p
12			VDDMN	subpull.seq.pro
	Majority			
	90	100	110	120
81	IPGNPSQVGIIVRTQD	WTKDVSADRYIDLSK	NEVWL	pullseqsig.seq.PRO
68	IAGITSSSAADYSSKNLYLWNN	ETCDALSAPVADW	NDVST	klebpnseqsig.seq.p
17	I	ITVLI	PAEQ	subpull.seq.pro
	Majority			
	130	140	150	160
118	VEGNSQIFYN	EKDA	EDAAKPAVS	SNAYLDASNQVLVKLSQP
108	TPSGSDKYGPY	WVPIPLN	KESG	CINVI
30				MTTP
	Majority			
	170	180	190	200
158	LTLEGE	GSFTVHDDTANKD	IPVTSVKDAS	LGQDVTAVLA
145	DLRVA	FGDFT	DRTVSV	IAGNSAVYDSRADAFR
34	FRLETE	ITDF	PLAVREEYS	L
	Majority			
	210	220	230	240
198	GTFQHI	FGSDWAPDNHSTLL	KKVTNNLYQ	FSGDL
177	AAF	GVALAEAHWV	DKNTLLWPGGQ	DKPIVRLY
54				
	Majority			
	250	260	270	280
233	PEGNYQYKVAL	NDNSWNNPSYP	SDNINLTV	PAGGAHVTF
209	YSHSSKVAAD	GEGKFTDRYL	KLTPPTVS	QQVSMRF
54	EAKYKY		VCVSDHP	VTFGK
	Majority			
	290	300	310	320
273	IPSTHAVYDT	INNPNADLQVES	GVKTDLVT	TLGEDPDVS
244	PH	LSSYA	AFKLPD	NANVDELLQGETVAIAAAEDGILI
72	IHC	VRA		SSGHKTDLQIGAV
	Majority			

FIGURE 2A

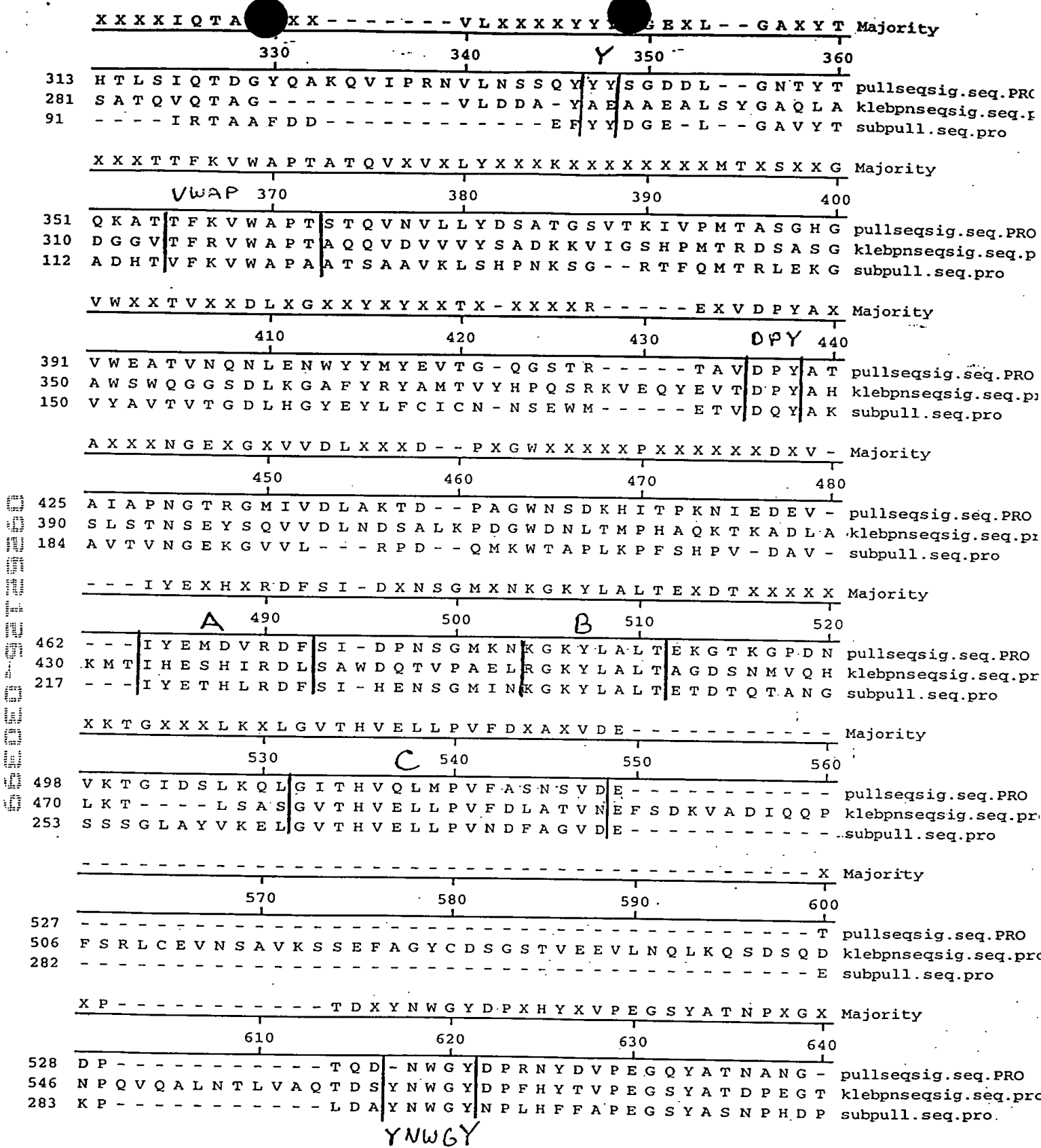


FIGURE 2B

X T R I K E F K X X X L H Q X - G X X V I M D V V Y T X A X X X S D - - Majority

650 660 670 680

555 N A R I K E F K E M V L S L H R E - H I G V N M D V V Y N H T F A T Q I S D - - pullseqsig.seq.PRO
586 - T R I K E F R T M I Q A I K Q D L G M N V I M D V V Y N H T N A A G P T D R T klebpnseqsig.seq.p:
312 Q T R K T E L K Q M I N T L H Q H - G L R V I L D V V F N H V Y K R E N S P - - subpull.seq.pro

- - F D K I V P X Y Y X R X X E X X X X X X X X X X D X A X E R R M X X K F Majority

690 700 710 720

592 - - F D K I V P E Y Y Y R T M I Q V I I P T D Q V L E M K L X A E R P M V Q K F pullseqsig.seq.PRO
625 S V L D K I V P W Y Y Q R L N E T T G S V E S A T C C S D S A P E H R M F A K L klebpnseqsig.seq.p:
349 - - F E K T V P G Y F F R H D E C G M P S N G T G V G N D I A S E R R M A R K F subpull.seq.pro

I A D S L X Y W X X E Y X I D G F R F D L M G X L X K D T X L X A X E X X X A X Majority

730 740 750 760

630 I I D S L K Y W V N E Y H I D G F R F D L M A L L G K D T M S K A A S E L H A I pullseqsig.seq.PRO
665 I A D S L A V W T T D Y K I D G F R F D L M G Y H P K A Q I L S A W E R I K A L klebpnseqsig.seq.p:
387 I A D C V V Y W L E E Y N V D G F R F D L L G I L D I D T V L Y M K E K A T K A subpull.seq.pro

N P G I X L F G E G W D X X T S X X X E X X X A X X X A X K G X G I G X F N D X Majority

770 780 790 800

670 N P G I A L Y G E P W T G G T S A L P D D Q L L T K G A Q K G M G V A V F N D N pullseqsig.seq.PRO
705 N P D I Y F F G E G W D S N Q S D R F E - - I A S Q I N L K G T G I G T F S D R klebpnseqsig.seq.p:
427 K P G I L L F G E G W D L A T P L P H E Q K A A L A N A P R M P G I G F F N D M subpull.seq.pro

L R D A V X G N X - F D S X A - - - - Q G F A X G A G X L X X A X - - - - Majority

810 820 830 840

710 L R N A L D G N V - F D S S A - - - - Q G F A T G A T G L T D A I - - - - pullseqsig.seq.PRO
743 L R D S V R G G G P F D S G D A L R Q N Q G I G S G A G V L P N E L A S L S D D klebpnseqsig.seq.p:
467 F R D A V K G N T - F H L K A - - - - T G F A L G N G E S A Q A V - - - - subpull.seq.pro

- - - - - X X G X A G S - - - - - X X X K - - - - - A Majority

850 860 870 880

738 - - - - - K N G V E G S - - - - - pullseqsig.seq.PRO
783 Q V R H L A D L T R L G M A G N L A D F V M I D K D G A A K K G S E I D Y N G A klebpnseqsig.seq.p:
495 - - - - - M H G I A G S - - - - - S G W K - - - - - A subpull.seq.pro

X X X X X X X P X E X I N Y V X S H D N X T L W D K I S X X X P Q E X D - A X R Majority

890 900 910 920

745 I N D F T S S P G E T I N Y V T S H D N Y T L W D K I A L S N P N D S E - A D R pullseqsig.seq.PRO
823 P G G Y A A D P T E V V N Y V S K H D N Q T L W D M I S Y K A S Q E A D L A T R klebpnseqsig.seq.p:
507 L A P I V P E P S Q S I N Y V E S H D N H T F W D K M S F A L P Q E N D - S R K subpull.seq.pro

X X M Q X L A X A X V M L X Q G V P F X Q X G X E X L R X K X G X X N S Y X S G Majority

930 940 950 960

784 I K M D E L A Q A V V M T S Q G V P F M Q G G E E M L R X K G G N D N S Y N A G pullseqsig.seq.PRO
863 V R M Q A V S L A T V M L G Q G I A F D Q Q G S E L L R S K S F T R D S Y D S G klebpnseqsig.seq.p:
546 R S R Q R L A V A I I L L A Q G V P F I H S G Q E F F R T K Q G V E N S Y Q S S subpull.seq.pro

FIGURE 2C

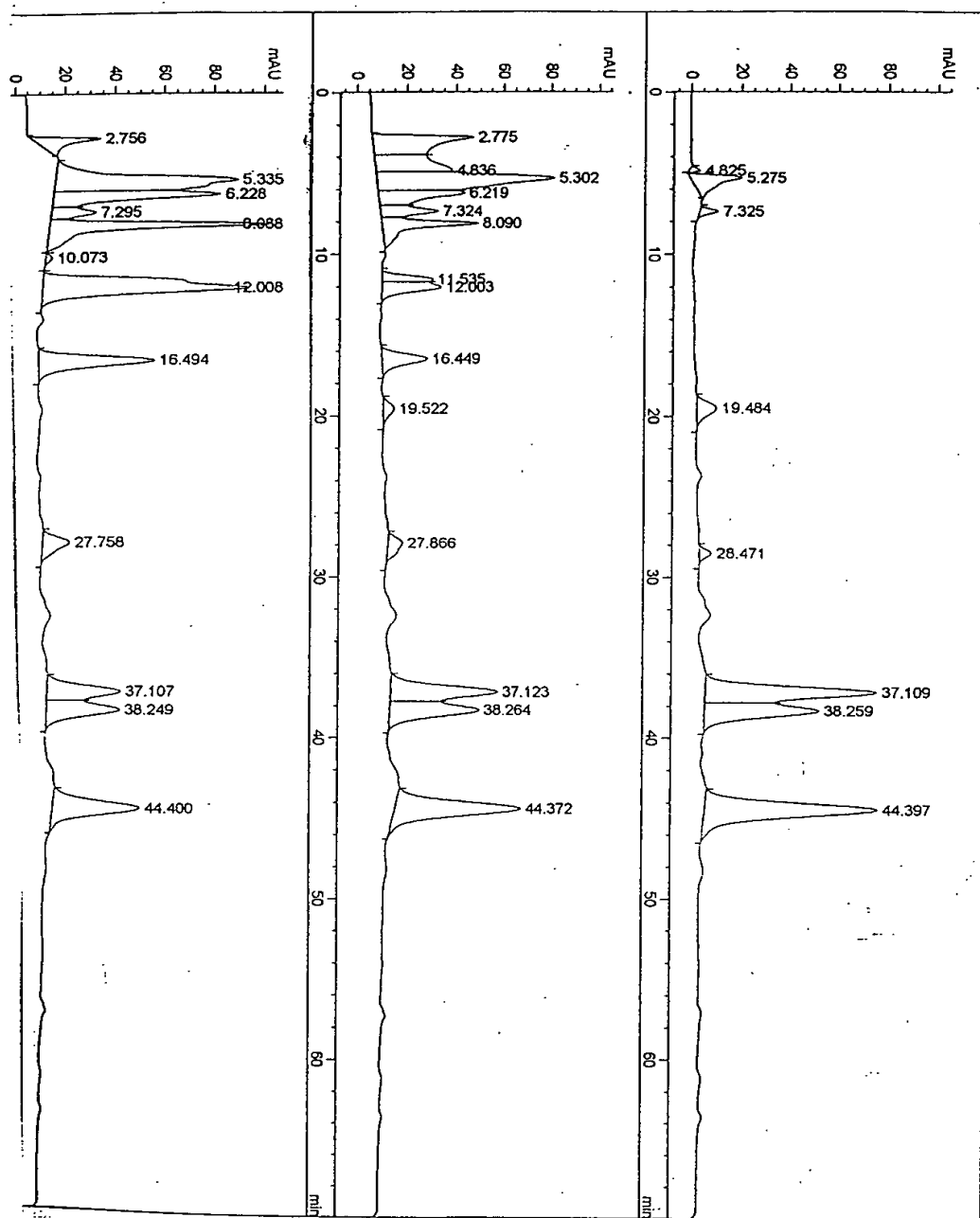


FIGURE 4 A, 4 B, 4 C

4 C

4 B

4 A

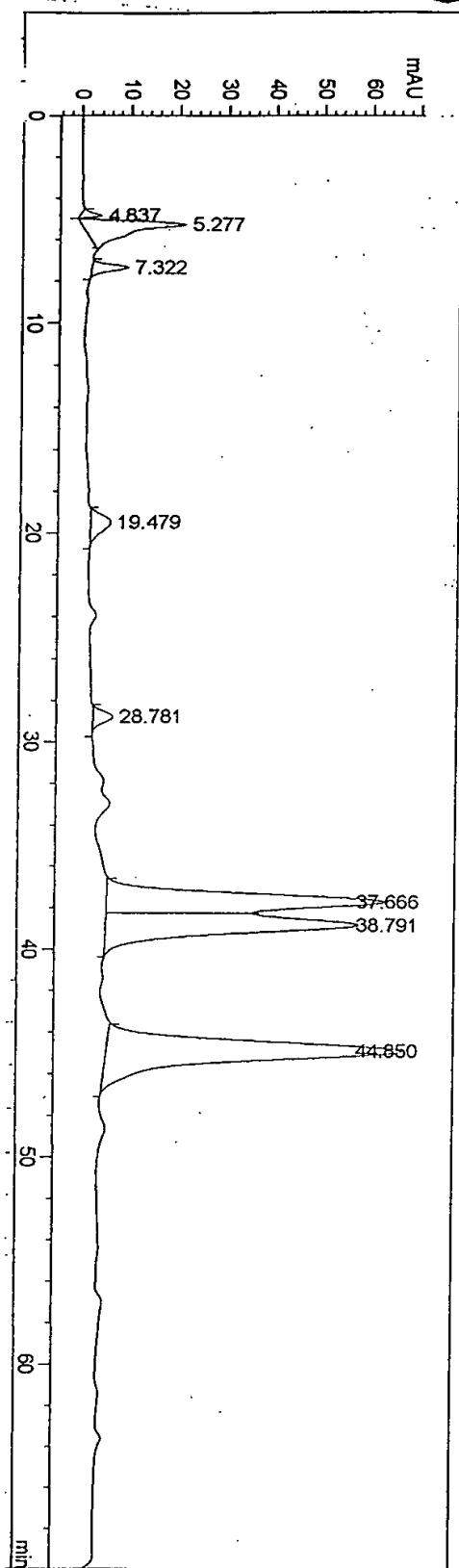


FIGURE 4 D

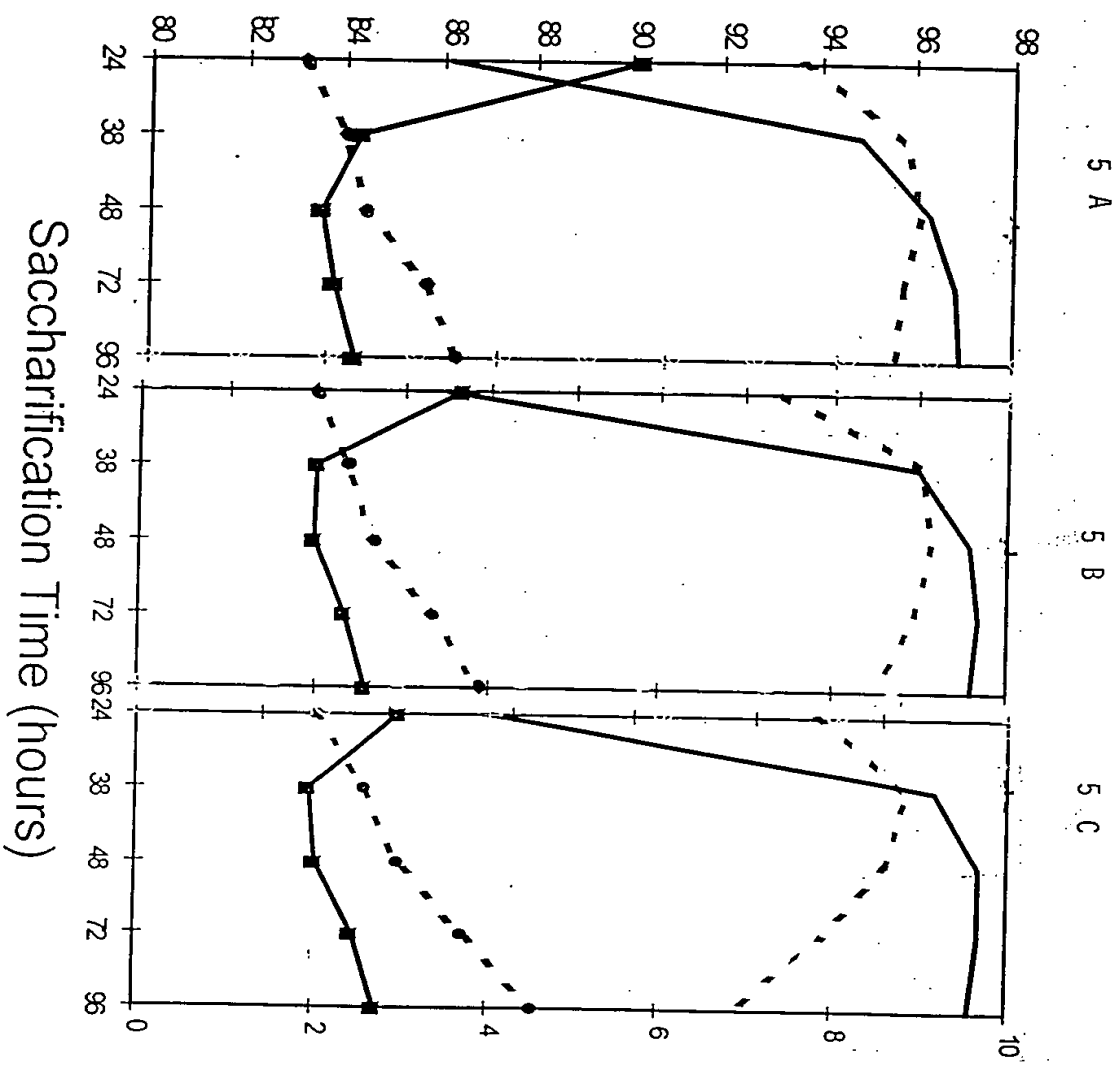


FIGURE 5 A, 5 B, 5 C

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[illegible]